

EcoR I

EcoR I

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|       |              |             |             |            |            |
|-------|--------------|-------------|-------------|------------|------------|
| -4152 | AGGAATTTCAT  | CCATTTAAAT  | CATACAATTT  | AATGGCTTTT | AGTATATTCA |
| -4102 | CAGGTTGTGC   | ATCCATCACA  | ATCCATTTTA  | GAACAGTTTT | ATTACTCCAA |
|       | <HNF-3/Fkh-1 |             | SREBP>      |            |            |
| -4052 | AAATAAAACCC  | TGCATTTCCTT | AGCCATCACC  | CCCCAACATC | CTCCATCCTC |
|       |              |             | NF-Y>       |            |            |
| -4002 | CTTCCAAGCC   | CTGGGCAACC  | ACCAATCTAC  | TTTCTGTCTC | TATAAATTTG |
| -3952 | CCAATTCTGG   | ACATTTTCATA | TAAATGGAAG  | CAAACAACAT | GTGAGACTTT |
|       | <NF-Y        | <IRF-2      |             |            |            |
| -3902 | GTGACTGGCT   | GCTTTTCACTT | AGCATTCTAT  | TTTAAAGGCT | CATTATGTTA |
| -3852 | CAGTACTTAG   | CAGTACTTCA  | TTC'TTTTTTA | TTCTCAAATG | GTATTCCACT |
| -3802 | GTGTGGGTAT   | CCCATATCAT  | ATTATTAGAG  | ACAGGTTCTC | ACTCTGTCAC |
| -3752 | CCAGGCTGGA   | GTGCAGTGGC  | ACAATCATAG  | CTCACTGTAA | CCTCAAACCT |
|       |              | <SREBP      |             |            |            |
| -3702 | CTGGGCTCAA   | GTGATCCTAC  | TACCTCAGCC  | TCCAGAGTAG | CTAGGACTAC |
|       |              |             |             |            | <IRF-1     |
| -3652 | AGGCACACAC   | AGCCATACCT  | GGCTAATTTT  | TTTTTTTAAT | TTTCATTTTA |
| -3602 | TGTATTCATT   | TTCTTTCTTT  | TTTGTTGTTG  | TTGTTTTGAG | ATAGGGTCTC |
| -3552 | ACTTTGTTAC   | CCAGGCTGGA  | GGGCAGTGGC  | ATGGTGACAG | CTGAGCAGCC |
|       |              | <SREBP      |             |            |            |
| -3502 | TTGACTTCCT   | GGGCTCAAGT  | GATCCTCCTG  | CCTCAGCCTC | CCAAGTAGCT |
| -3452 | GGGACTACAA   | ACACGTGTCA  | CCATGCCTGG  | CTGATATTTT | TTTTCTTGAA |
| -3402 | ACAGGGTATC   | ACTCTGTTGC  | CCAGGCTGGA  | GTACAGTGGC | GTAATAATAG |
|       | c1           |             |             |            |            |
|       | Pst I        |             |             |            |            |
|       | ~~~~~        |             |             |            |            |
| -3352 | CTCACTGCAG   | CTTCCCCTCC  | TGGGCTCAAG  | CAATCCGCTG | GCCTCAGCAT |
| -3302 | CCTGAGTAGC   | TGGGACTACA  | GGCTTG TGCC | ACCAGGCCCA | GCTAAGTTTT |
| -3252 | AAAAAATGAT   | TTTTTGGTATA | GAGGAGGTCT  | TGCTATGTTG | CTCAGGCTGT |
|       |              |             |             |            | SREBP>     |
| -3202 | ATTTTTTATTG  | TTGAGACAAG  | GTCTCACTAT  | GTTGCCATGA | TCCCCCACC  |
|       |              |             |             | <AP-1      |            |
| -3152 | TCCACTTCCC   | AAAGTGCTCA  | TCTTATCTGT  | TCATTAGTCA | GTTGACAGAC |
|       |              |             | <RAR-α1     |            |            |
| -3102 | ATTTAGGTTG   | TTTCCACTTT  | TTGACCATTA  | TGAATAATAC | TCCAGTGAAT |
| -3052 | ATTTCATGTAT  | ACATTTGTGT  | GGGCATATGT  | TTTCATTTCT | GTTGGGTTTA |
| -3002 | TATCTAGGAG   | TGGAATTGCT  | GGATCCCGGG  | TAATATTTTG | ACAGGCAGAG |
|       |              |             |             | C/EBP-β>   |            |
| -2952 | TTCAGGGGAA   | GAAAAACTTG  | GGAAAATGAA  | GCATGTTTAG | AAATCAGCAA |
| -2902 | GAGTGCAGGG   | GTTTTTCGGA  | GTTTTATTTT  | ATATTCTGTT | GACAAATGTG |
| -2852 | CAGTTTGATG   | AAGATACAAG  | TTATACTAAG  | TGAGAAGTCA | GAATTAAGGC |
| -2802 | TGGAATAGGG   | CGTTCAGAGT  | AAAATCATGA  | AGCACTTTGA | ATACCAAAT  |
|       |              | NF-1>       | <HNF3-β     |            |            |
| -2752 | TAAGGAGCTT   | GGCTGTAAAC  | AAAATAATAA  | AAAATCACAA | TTTTTTTTTT |
| -2702 | TTTTTTTGAGA  | AAGAGTCTTG  | CTCTTTCACC  | CTGGCTGGAG | GGCAGTGGTG |
|       | <SREBP       |             |             |            |            |
| -2652 | TGATCTCAGC   | TCACTGCAAC  | TTTCGCCTCC  | CGGGTTCAAG | CAATTCTCCT |

Figure 1, page 2

<NF-kB

-2602 GCTTCAGCCT CCCAAGTAGC TGGGACTACA GGCACTCCC ACCATGCCCA  
NF-kB><IRF-1

-2552 GCTGATTTTT GTATTTTTAG TAGAGATGGG ATTTCACTTT GTTGGCCAAG

-2502 CTGGTCTCAA ACTTTTTGCT GTCATAATTG TTGTAAGTAT TGTTCTTTTT

AP-2> <HNF3-β

-2452 GCTGAGGTAG GGCCCCCAGA CCAAAAAAAAA TAAATCCTAG AATCCAAATC

-2402 AGTGTGTTGG TTTGACCACT GTCACTTGAG AACCACAGTG TGACCAGGGC

C2  
Taq I

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-2352 CTCAGGAGTA GAGGTGATCT CTGCTCGAAA GAGAAATAGA ATGAAAATAT

<Whn

-2302 TCTCCGGGCC AGGCGTGGTG GCTCATGCCT GTAATCCCAG CACTTTGGGA

T3R>

SREBP> RAR-α1>

-2252 GGCCAAGGCA TGTGSATCAC CTGAGGTCAG GAGTTCAAAA CCAGCCTGGC

-2202 CAACATGGTG AAACCCCGTC TCTACTAAAA ATACAAAAAA TTAGCTAAGT

-2152 GTGGTGGCGC ATGCCTGTAA TCCCAGCTAC TTGGGAGGGT GAGGCAGGAG

<Pax-6 SREBP>

-2052 AATTTCTTGA ACCCGGGAGG CAGAGGTTGC AGTGAAGCGA GATCACACCA

<AP-2 <HNF-3/Fkh-2

-2002 CTGCACTCCA GCCTGGGGGA GAGAGCGAGA CTTCTCTCTCA AAAAACAAA

C/EBP-β> <CHOP

-1952 AAACAAAAGA ATTAAGCAA TTAGACATTG CAGAGAGAAC CTGAAGGGGG

RAR-α1> <NF-1 Pax-6>

-1902 TCAGACCACG TACAGATTTC TGTGCCACAT GCCAAGTACT TCTGAGGCAT

-1852 GACTGGATGA GCTGTCCACA TCTGAAATCA TCCAGTCTTG TTCAGAACTT

RAR-α1>

-1802 TCACACCGGA CAGGGAGCCA GGAAGTGAAT GCAGTCTCCT GGTCACTGGC

NF-1> <ER <NF-1

-1752 CAGAGAGTTG GCCTTGACCC TGAGACCAGT GGCCAACAAA GGAGCTGCTT

<Rel AP-1>

-1702 AGTCTACCTC CCAGGAAATC CCAGGTGCTT GTCTTCTCTGG GAAGTGAATC

<NF-1

-1652 ATTGGCGCAG CACTCCGTAT TTTCTCCTCT TCCCAGGGGA AGGATCCTAG

<GR

-1602 GGCAGTATTT GGGAAAGACA TGGGCATGGA AGGACACCGG GTGAATGCAT

C3
Sac I

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-1552 AGCCTGCCTG GTTCTGAGCT CTCATGGTAA GGCTCCTACA GACACGGAAA

-1502 AGATGGGGGC ACAGGGACAG ATCAGTAGGG TCAGAGCATC TCAGGGACCG

-1452 AGGGCAATAT GGTCCTGAGC AGGGATTAAG AGCTTGGGCT CTCATATGCT

<CREB <ER

-1402 GTTTCTGGGC TCAACTGCCA GCTCCGTCAC TTAGTGGTTG CTGTGACCAT

-1352 GGGCAAGTTA TTCCATCTCT CCATATCTCT TTCCTCACTT TTAAATGGA

Scyb  
B2

1000 900 800 700 600 500 400 300 200 100 0

Figure 1, page 3

c4  
Kpn I  
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-1302 ATAATGGGGT ACCCACCTCC CAGGGTCACA GAGAGGCTTA CAGAAAACGA
NF-1>

-1252 TTCTTGTGAA TTGGCTTGCA GTAATAATTC AATACCTGCC AGCTATTCTT
<PPAR-α <Oct-1

-1202 ATTCCACATC CAAGCCCTTT CGCCTGCTGC TGGGTGAAAA CACATGTCAG
CREB/ATF> <STAT <C/EBP-β

-1152 TGTTCCTGA CGGTTCAC AAAGAAGATT CCAAAATTAC AACCTGCCAG

-1102 TCTGAAGAAT CTCCAAAACA TCCCGCACGC ATCCTGGAGG CGCGGGCTTG
<SP-1

NF-kB> <NF-kB
-1052 GGGATGGGAC TGCCCGCCCCG GGTCTGAAC AGGATGCGTG CGCGCAGGCA
Ets-1>

-1002 CACACACACC AGCCAGCCTG TGTGTGCGGC CGGAGTCCGG TCGGTCCCCG
<Myc/Max
<Whn SP-1>

-952 GGTGAGCAGC GCGTGGCTGG TGGGCGGGGC AGAGCCATTG TTCGCAGGCG
c5
Sma I
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-902 TACCGAGCCC CCCGCGCTCG CCCGGGAGGG AGGCGGGGCT TCCCGCGTCC  
NF-kB> <NF-kB<Whn  
Myc/Max>  
Whn>

-852 CCAAGCTCCA GATCCTGGGG TGGCTGCCAC GTCTCCCTGC CACGCGCCTG  
<AP-2 c8

-802 GGGGGACGGG AAGACGGGAC GGAGATGTTA GTGGTGGGCG CCCCCGAGG  
<RFX-1 RFX-1> NF-kB>

-752 GTTCACTACT GTTTCCTGAG AAACTTCCCC AGTGCCCACC CACCCGTTCT  
AP-2>

-702 CCGTGTGCCC GAGGGCCGGT CCTGGGCTAG GCTCCGCGCC CCAGCCCCAA  
Whn> c9

-652 ACCGGGTCCC CAGCCCCTTC CAGAGAGAAA GCTCCCGACG CGGGATGCCG  
AP-2> ISRE>

-602 GGCAGAGGCC CAGCGGCGGG TGGAAGAGAA GCTGAGAAGG AGAAACAGAG  
SP1> RFX1> SREBP>

-552 GGGAGGGGGA GCGAGGAGCT GCGGCAGAG GGAACAGCAG ATTGCGCCGA  
<NF-1  
c6 NF-Y>  
Eae I CREB>  
~~~~~ AP-1>

<NF-1 c10
NF-Y> RFX-1>

-502 GCCAATGGCA ACGGCAGGAC GAGGTGGCAC CAAATTCCTT TCGGCCAATG
<C/EBP-β <Oct-1 GC box>

-452 ACGAGCCGGA GTTTACAGAA GCCTCATTAG CATTTCCCCA GAGGCAGGGG
EBV>

-402 CAGGGGCAGA GGCCGGGTGG TGTGGTGTCT GTGTCGGCAG CATCCCCGGC

[illegible]

Sub
A6

[illegible]

Sub ~~AC~~

[illegible]

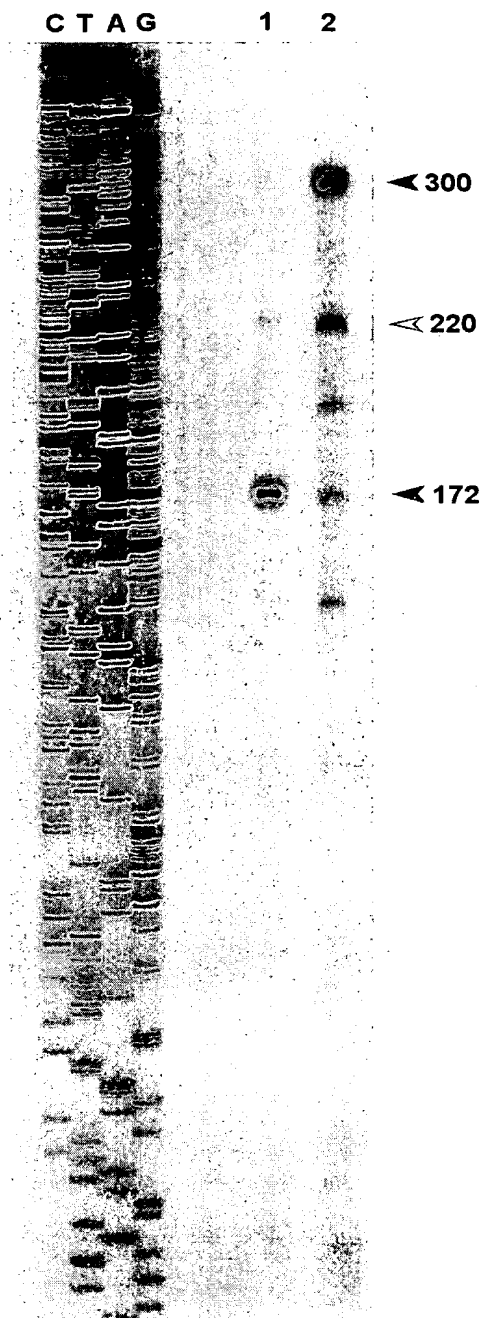
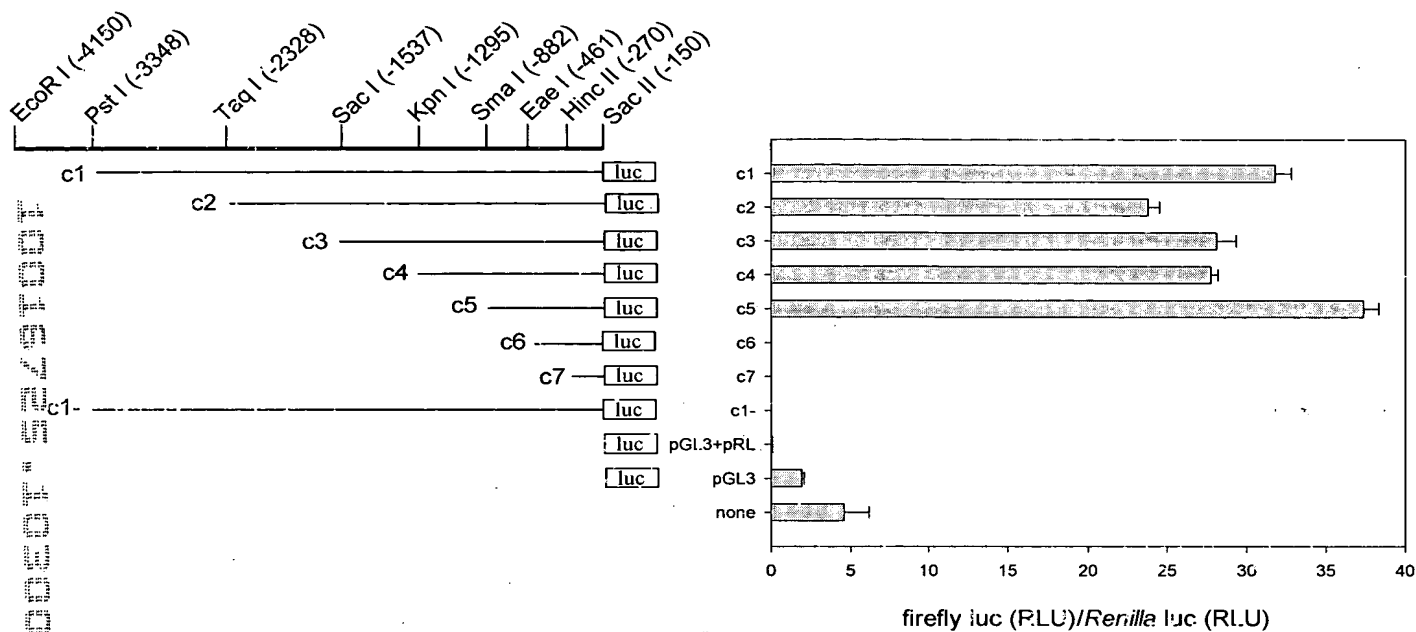


Figure 3

Figure 4



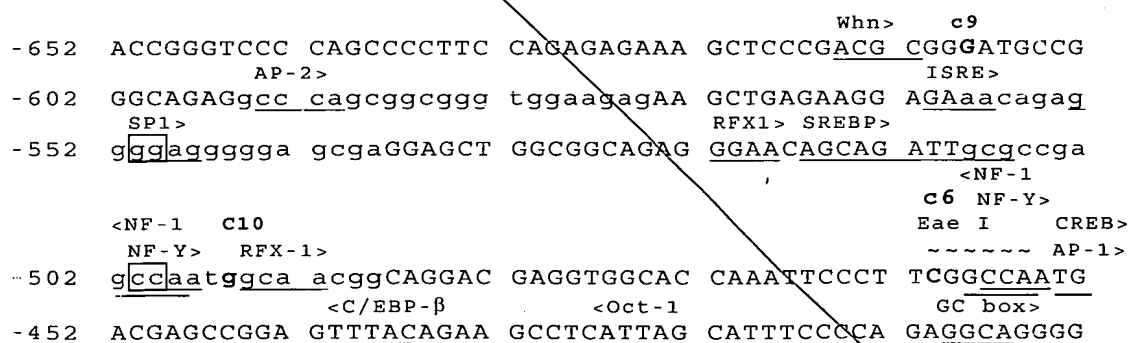
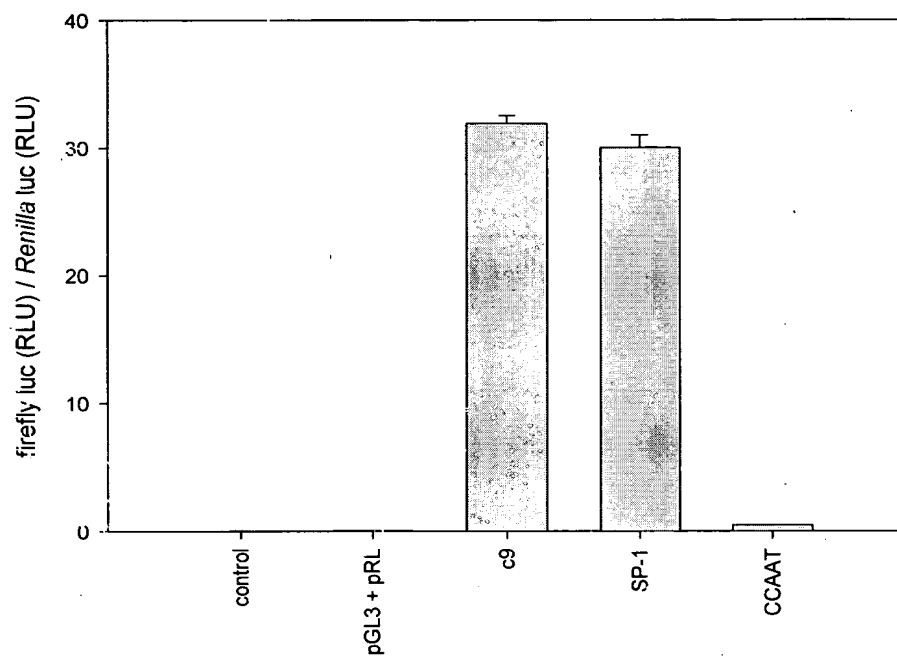


Figure 5

Figure 6



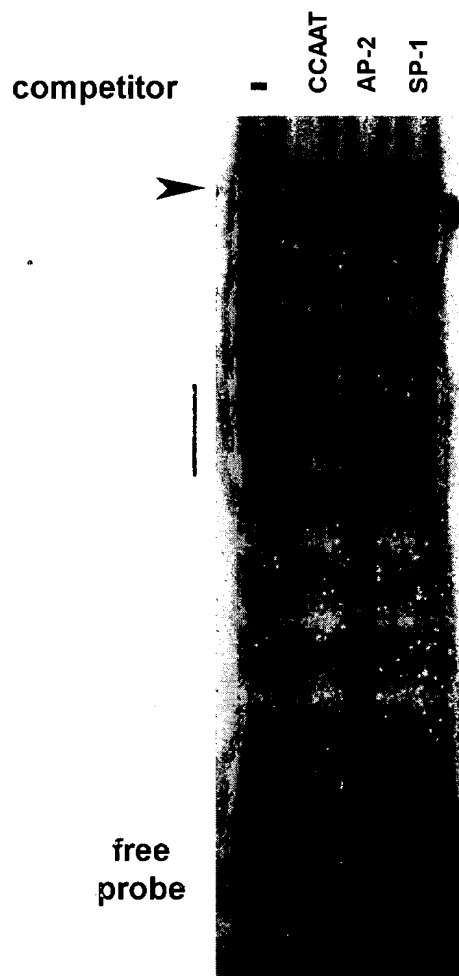


Figure 7

AP-4>
IK2> **SRE**>
RFX-1>

IK2>

mSCD1 (-610) GGGAGGAGAGACGGAGAAGCTAGAGGCAGAGGGAAC**AGC**
 : : : : :
mSCD2 (-487) GGGAGGAGGGGGGGCGGAGCTGGAGGCAGAGGGAAC**AGC**
 : : : : :
hSCD (-552) GGGAGS-GGGAGCGAGGAGCTGGCGGCAGAGGGAAC**AGC**

CCAAT>
NF-Y>
<NF-1
<ΔEF-1

mSCD1 (-571) **AGATTGCGCCTAGCCCAATGGAAAAGGCAGGACAAGGTGG**
 : : : : :
mSCD2 (-448) **AGATTGTGCAGAGCCAATGAGAGCAGCAGGACGAGGTGG**
 : : : : :
hSCD (-514) **AGATTGCGCCGAGCCAATGGCAACGGCACGACGAGGTGG**

Sub
A6

[illegible]

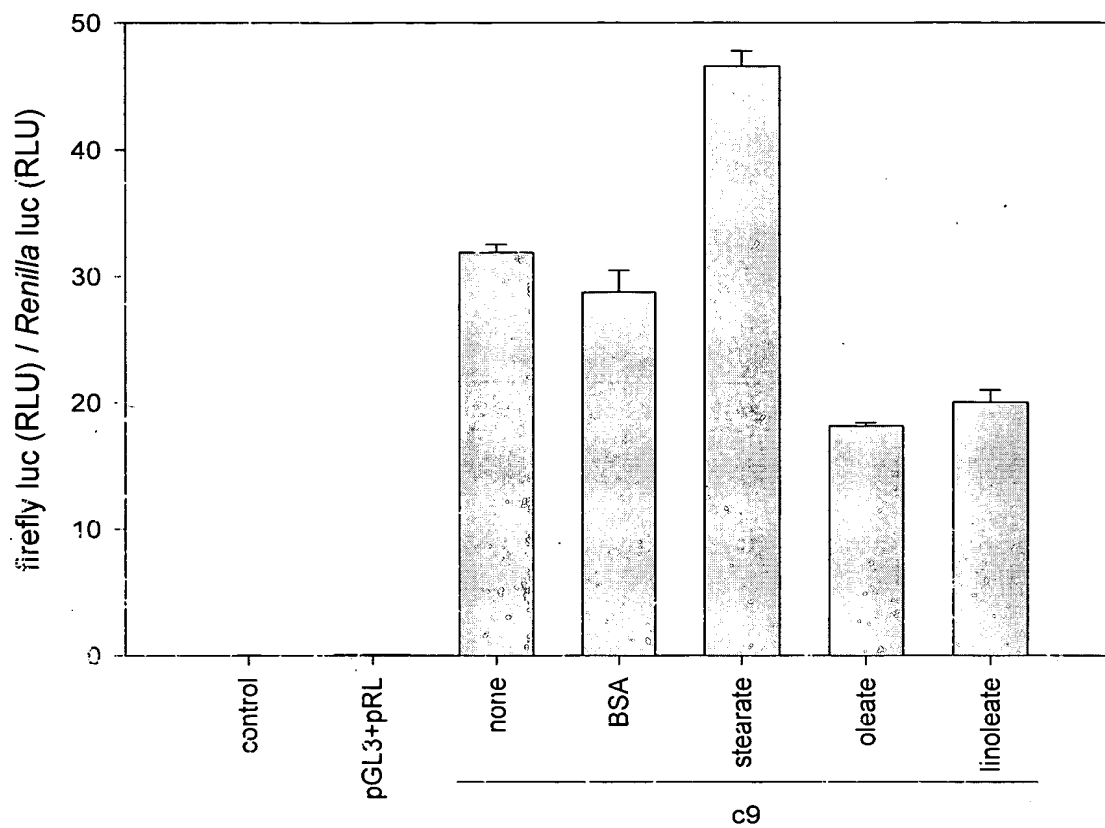


Figure 9